

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:47:04 ; Search time 16 Seconds
(without alignments)
48.096 Million cell updates/sec

Title: SEQ3
Perfect score: 43
Sequence: 1 qppraaiy 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 605

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	19	44.2	7	S71299	ICL2 protein - Par
2	19	44.2	7	PT0283	Ig heavy chain CRD
3	16	37.2	5	B37988	acid proteinase li
4	16	37.2	8	B24749	neuropeptide B - b
5	16	37.2	8	B39745	endoglycosylcerami
6	15	34.9	7	A61081	tryptophyllin, bas
7	15	34.9	7	A39690	neural cell adhesi
8	15	34.9	7	S15597	orf 4 rara 5'-regi
9	14	32.6	8	S16324	hypothetical prote
10	14	32.6	8	S21288	lectin - potato (f
11	14	32.6	8	PT0030	inulinase (EC 3.2.
12	14	32.6	8	E47393	neuropeptide calla
13	14	32.6	8	S10783	enamelin f - bovin
14	14	32.6	8	PT0559	T-cell receptor be
15	13	30.2	8	S22428	chitin-binding pro
16	13	30.2	8	S14895	apolipoprotein A-I
17	12	27.9	4	A02147	phagocytosis-stimu
18	12	27.9	5	B22565	R-phycocerythrin al
19	12	27.9	6	B60110	repetitive protein
20	12	27.9	6	A11490	pyruvate kinase (E
21	12	27.9	6	PT0618	T-cell receptor be
22	12	27.9	7	A44428	platelet aggregati
23	12	27.9	7	PC1316	large granule L3 c
24	12	27.9	7	S42620	aggreacan - bovine
25	12	27.9	7	A58718	carnocin UR49 - Ca
26	12	27.9	8	S43971	tumor-associated a
27	12	27.9	8	A23967	leucopyrokinin - M
28	12	27.9	8	S66646	cardioacceleratory
29	12	27.9	8	A14683	aspartate transami

30	12	27.9	8	2	A61457	penalbumin - Adeli
31	12	27.9	8	2	PT0691	T-cell receptor be
32	12	27.9	8	2	A39690	neural cell adhesi
33	11	25.6	3	3	A33802	thyrotropin-releas
34	11	25.6	3	3	S68328	blood cell protein
35	11	25.6	5	2	JN0860	peptidyl-dipeptida
36	11	25.6	5	2	P50324	ribulose-bisphosph
37	11	25.6	5	2	S55237	zinc-binding prote
38	11	25.6	5	3	UT0870	phytosulfokine alp
39	11	25.6	6	2	S66195	alcohol dehydrogen
40	11	25.6	6	2	A37765	hypothetical prote
41	11	25.6	6	2	PC4127	hypothetical 6 pro
42	11	25.6	6	2	A19780	transferrin - bovi
43	11	25.6	7	1	NYPG7	hypothalamic hepta
44	11	25.6	7	2	A25269	sex pheromone cAm3
45	11	25.6	7	2	PH0932	T-cell receptor be

ALIGNMENTS

RESULT 1

S71299 ICL2 protein - Paramaecium tetraurelia (fragment)
C:Species: Paramaecium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
C:Accession: S71299
R:Madaddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
Eur. J. Biochem. 238, 121-128, 1996
A:Title: Characterization of centrin genes in Paramaecium.
A:Reference number: S71298; MUID:96248429; PMID:8665928
A:Accession: S71299
A:Molecule type: protein
A:Residues: 1-7 <MAD>
A:Experimental source: strain d4-2
C:Genetics:
A:Genetic code: SGC5

Query Match 44.2%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
DB 2 QPP 4

RESULT 2

PT0283 Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0283
R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0283
A:Molecule type: DNA
A:Residues: 1-7 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 44.2%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
DB 5 QPP 7

RESULT 3

B37988
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
C:Species: Physarum polycephalum
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C:Accession: B37988
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og
J. Biol. Chem. 265, 19898-19903, 1990
A:Title: Purification and characterization of a novel intracellular acid proteinase from
A:Reference number: A37988; MUID:91060608; PMID:2246266
A:Accession: B37988
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <MUR>

Query Match 37.2%; Score 16; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
: ||
DB 2 EPP 4

RESULT 4
B24749
neuropeptide B - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
C:Accession: B24749
R:Yang, H.Y.T.; Pratta, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b
A:Reference number: A94074; MUID:86067985; PMID:3865193
A:Accession: B24749
A:Molecule type: protein
A:Residues: 1-8 <YAN>
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide

Query Match 37.2%; Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPR 4
: ||
DB 4 QPQR 7

RESULT 5
B39745
endoglycosylceramidase (EC 3.2.1.123) I - Rhodococcus sp. (fragment)
C:Species: Rhodococcus sp.
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 31-Dec-1993
C:Accession: B39745
R:Ito, M.; Ikegami, Y.; Yamagata, T.
J. Biol. Chem. 266, 7919-7926, 1991
A:Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosylceramidases. El
ble using these activator proteins.
A:Reference number: A39745; MUID:91210321; PMID:1850427
A:Accession: B39745
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <ITO>
C:Keywords: glycosidase; hydrolase

Query Match 37.2%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PRA 5
: ||
DB 6 PRA 8

RESULT 6

A61081
tryptophyllin, basic - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C:Accession: A61081
R:Montecucchi, P.C.; Vincenti, M.; Lazzarini, A.M.; Rusconi, L.; Erspamer, V.
Int. J. Pept. Protein Res. 33, 391-395, 1989
A:Title: Isolation, structure determination and synthesis of a novel tryptophan-containi
A:Reference number: A61081
A:Accession: A61081
A:Molecule type: protein
A:Residues: 1-7 <MON>
C:Comment: The biological activity of this peptide was not determined.
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; hydroxyproline; skin
F:3/Modified site: 4-hydroxyproline (Pro) #status experimental
F:7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 34.9%; Score 15; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
: ||
DB 1 KPP 3

RESULT 7

A39690
neural cell adhesion molecule, cardiac splice form -, -, -, - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: A39690
R:Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule nR
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: A39690
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-7 <REY>
A:Cross-references: GB:M63970
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 34.9%; Score 15; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPR 4
: ||
DB 1 QPVR 4

RESULT 8

S15597
orf 4 rara 5'-region - human
C:Species: Homo sapiens (man)
C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C:Accession: S15597
R:Brand, N.J.; Petkovich, M.; Chambon, P.
Nucleic Acids Res. 18, 6799-6806, 1990
A:Title: Characterization of a functional promoter for the human retinoic acid receptor-
A:Reference number: S15594; MUID:91088249; PMID:2175878
A:Accession: S15597
A:Molecule type: DNA
A:Residues: 1-7 <BRA>
A:Cross-references: EMBL:X56058; NID:g35876
A:Note: This ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0
C:Comment: This sequence is not thought to be translated.
C:Genetics:
A:Gene: GDB:RARA

A;Cross-references: GDB:120337; OMIM:180240
A;Map position: 17q12-17q12

Query Match 34.9%; Score 15; DB 4; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PRAAI 7
|||
Db 2 PRGGV 6

RESULT 9

S16324
hypothetical protein 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C;Accession: S16324
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A;Title: A novel class of plant proteins containing a homeodomain with a closely linked
A;Reference number: S16323; MUID:91266907; PMID:1675603
A;Accession: S16324
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <RUB>
A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g57259

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
|||
Db 7 PP 8

RESULT 10

S21288
lectin - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
C;Accession: S21288
R;Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Siabias, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1992
A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
A;Reference number: S21288; MUID:92272683; PMID:1590771
A;Accession: S21288
A;Molecule type: protein
A;Residues: 1-8 <ML>
A;Experimental source: var. Ulster Sceptre
C;Function:
A;Description: may be involved in defence mechanism of the plant
C;Keywords: hydroxyproline; lectin

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
|||
Db 7 PP 8

RESULT 11

PT0030
inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)
N;Alternate names: inulase
C;Species: Aspergillus ficuum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
C;Accession: PT0030
R;Etcalibi, M.; Baratti, J.C.
Agric. Biol. Chem. 54, 61-68, 1990

A;Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.
A;Reference number: PT0030; MUID:90344234; PMID:1368526
A;Accession: PT0030
A;Molecule type: protein
A;Residues: 1-8 <FTT>
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPR 4
|||
Db 5 QPYR 8

RESULT 12

E47393
neuropeptide callatostatatin 5 - bluebottle fly (Calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
C;Accession: E47393
R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A;Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequence
A;Reference number: A47393; MUID:93211980; PMID:8460157
A;Accession: E47393
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <DUV>
A;Experimental source: whole flies
A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
|||
Db 2 PP 3

RESULT 13

S10783
enamelin f - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Accession: S10783
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albi
A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10783
A;Molecule type: protein
A;Residues: 1-8 <STR>
C;Keywords: enamel; phosphoprotein

Query Match 32.6%; Score 14; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PP 3
|||
Db 4 PP 5

RESULT 14

PT0559
T-cell receptor beta chain V-D-J region (126-1BH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0559
R;Peeney, A.J.

J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: F0509; MUID:91277601; PMID:1711558
 A;Accession: F0559
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-8 <PEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 32.6%; Score 14; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 pp 3
 ||
 Db 4 pp 5

RESULT 15
 S22428
 chitin-binding protein - potato (fragment)
 C;Species: Solanum tuberosum (potato)
 C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
 C;Accession: S22428
 R;Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
 Biochem. J. 283, 813-821, 1992
 A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
 A;Reference number: S21286; MUID:92272683; PMID:1590771
 A;Accession: S22428
 A;Molecule type: protein
 A;Residues: 1-8 <ML>
 C;Function:
 A;Description: may be involved in plant defence
 C;Keywords: glycoprotein; hydroxyproline

Query Match 30.2%; Score 13; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PRAAY 8
 | : |
 Db 1 PXDMVY 6

Search completed: July 28, 2004, 07:55:22
 Job time : 16 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:17:39 ; Search time 13 Seconds
(without alignments)
32.043 Million cell updates/sec

Title: SEQ3
Perfect score: 43
Sequence: 1 qppraaiy 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	16	37.2	8	1 NPMB_BOVIN	P15507 bos taurus
2	15	34.9	7	1 TPFY_PACDA	P83455 pachymedusa
3	15	34.9	7	1 UPO6_MOUSE	P38642 mus musculus
4	15	34.9	8	1 PPK2_PERAM	P82692 periplaneta
5	14	32.6	8	1 ALL5_CALVO	P41841 calliphora
6	12	27.9	4	1 TUFT_HUMAN	P01858 homo sapien
7	12	27.9	7	1 LANC_CARUI	P36960 carnobacter
8	12	27.9	8	1 FAR7_ASCSU	P43171 ascaris suu
9	12	27.9	8	1 LMT2_LOCOMI	P22396 locusta mig
10	12	27.9	8	1 LPK_LEUMA	P13049 leucophaea
11	12	27.9	8	1 PPK3_PERAM	P82618 periplaneta
12	12	27.9	8	1 RS7_MYCIT	P33564 mycobacteri
13	12	27.9	8	1 UC25_MAIZE	P80632 zea mays (m
14	12	27.9	8	1 UPAT_HUMAN	P30087 homo sapien
15	11	25.6	5	1 PSK_DAUCA	P58261 daucus caro
16	11	25.6	7	1 CIA_ENTFA	P11932 enterococcu
17	11	25.6	7	1 B105_LITRU	P82101 litoria rub
18	11	25.6	7	1 HV7_PIG	P01153 sus scrofa
19	11	25.6	8	1 UH05_RAT	P56575 rattus norv
20	10	23.3	3	1 THYL_PIG	P01151 sus scrofa
21	10	23.3	8	1 ANG2_BOTJA	Q10582 bothrops ja
22	9	20.9	7	1 ALL3_CARMA	P81806 carcinus ma
23	9	20.9	7	1 ALL4_CARMA	P81807 carcinus ma
24	9	20.9	7	1 ALL5_CARMA	P81808 carcinus ma
25	9	20.9	7	1 MNP1_LEPDE	P42984 leptinotars
26	9	20.9	7	1 TV51_LITRU	P82055 litoria rub
27	9	20.9	7	1 UN06_PINPS	P81675 pinus pinas
28	9	20.9	8	1 ALL6_CYPDO	P82157 cydia pomon
29	9	20.9	8	1 ALL7_CARMA	P81809 carcinus ma
30	9	20.9	8	1 ALL8_CARMA	P81811 carcinus ma
31	9	20.9	8	1 ALL9_CARMA	P81812 carcinus ma
32	9	20.9	8	1 LCK8_LEUMA	P19990 leucophaea
33	9	20.9	8	1 NS3_MYCTU	P81152 mycobacteri

34 9 20.9 8 1 UPO6_MOUSE P38644 mus musculus
35 8 18.6 5 1 SUGA_ACHDO P19991 acheta dome
36 6 18.6 6 1 OVM_LEPDE P42985 leptinotars
37 8 18.6 7 1 ALL7_CYPDO P82158 cydia pomon
38 8 18.6 7 1 FAR4_PANRE P41875 panagrellus
39 8 18.6 7 1 UH11_RAT P56575 rattus norv
40 8 18.6 7 1 ALL2_CARVA P81815 carcinus ma
41 8 18.6 8 1 ALL5_CARMA P81818 carcinus ma
42 8 18.6 8 1 ALL8_CARMA P81821 carcinus ma
43 8 18.6 8 1 ALL3_CYPDO P82154 cydia pomon
44 8 18.6 8 1 ALL4_CALVO P41840 calliphora
45 8 18.6 8 1 ALL4_CYPDO P82155 cydia pomon

ALIGNMENTS

RESULT 1
NPMB_BOVIN
ID NPMB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Morphine modulating neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.F., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: Modulates the action of morphine.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;
Query Match 37.2%; Score 16; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPFR 4
Db 4 QPQR 7
RESULT 2
TPFY_PACDA
ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trypophyllin-1 (pdt-1).
OS Pachymedusa dactylos (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
Chen T.B., Orr D.F., Shaw C.;

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RT "Pachymedusa daemnicolor tryptophyllin-1 (Pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA."
RL Submitted (SEP-2002) to Swiss-Prot.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:000576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 34.9%; Score 15; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
Db :||
1 KPP 3

RESULT 3
UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Sellkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 46 kDa.
FT NON_TER 7
FT SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 34.9%; Score 15; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPP 3
Db :||
2 KPP 4

RESULT 4
PPK2_PERAM STANDARD; PRT; 8 AA.
AC P26692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Psa-PK-2) (FXPR-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria."
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator and play
CC a role in the integration of information within the brain. May be
CC involved in the control of visceral muscles due to its ability to
CC behave as potent inhibitors of peristaltic movements. May also
CC fulfill a neurohormonal role on muscles of the gut and heart.
CC -!- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.
CC -!- SIMILARITY: Belongs to the allatostatin family.
DR Neuropeptide; Amidation; Hydroxylation.
KW PIR; E47393; E47393.
FT MOD_RES 3 3 HYDROXYLATION (20%).

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RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach."
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRlamides in the nervous system of
RT the American cockroach."
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 8 AMIDATION.
FT SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 34.9%; Score 15; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPRA 5
Db :||
2 PPFA 5

RESULT 5
ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatin."
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria."
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator and play
CC a role in the integration of information within the brain. May be
CC involved in the control of visceral muscles due to its ability to
CC behave as potent inhibitors of peristaltic movements. May also
CC fulfill a neurohormonal role on muscles of the gut and heart.
CC -!- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.
CC -!- SIMILARITY: Belongs to the allatostatin family.
DR Neuropeptide; Amidation; Hydroxylation.
KW PIR; E47393; E47393.
FT MOD_RES 3 3 HYDROXYLATION (20%).

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FT  MOD RES      8      8      AMIDATION
SQ  SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match      32.6%; Score 14; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 PP 3
Db  2 PP 3

RESULT 6
TUFT HUMAN
ID  _TUFT_HUMAN  STANDARD; PRT; 4 AA.
AC  P01855;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Phagocytosis-stimulating peptide (Tuftsin).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=72187087; PubMed=4112769;
RA  Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT  "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RL  Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN  [2]
RP  IMMUNOGLOBULIN CLASS.
RX  MEDLINE=68091045; PubMed=4169272;
RA  Fidalco B.V., Najjar V.A.;
RT  "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte.";
RL  Biochemistry 6:3386-3392(1967).
CC  -!- MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the
cell membrane of neutrophils in the blood. Leucokininase on the
membrane releases the active peptide tuftsin from the gamma chain.
CC  Tuftsin is essential for maximum stimulation of the phagocytic
activity of neutrophils.
CC  PIR; A02147; A02147.
DR  MIN; 191150; -.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006909; P:phagocytosis; NAS.
SQ  SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match      27.9%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PR 4
Db  3 PR 4

RESULT 7
LANC CARUI
ID  _LANC_CARUI  STANDARD; PRT; 7 AA.
AC  P36960;
DT  01-JUN-1994 (Rel. 29, Created)
DT  01-JUN-1994 (Rel. 29, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Lantibiotic carnocin U149 (Fragment).
OS  Carnobacterium sp. (strain U149).
OC  Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC  Carnobacterium.
CX  NCBI_TaxID=35782;
RN  [1]
RP  SEQUENCE.

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RX  MEDLINE=92321768; PubMed=1622206;
RA  Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA  Nes I.F.;
RT  "Purification and characterization of a new bacteriocin isolated from
a Carnobacterium sp.";
RL  Appl. Environ. Microbiol. 58:1417-1422(1992).
CC  -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
Active on Gram-positive bacteria.
KW  Antibiotic; Bacteriocin; Lantibiotic.
FT  NON_TER 7
SQ  SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match      27.9%; Score 12; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 QP 2
Db  5 QP 6

RESULT 8
FAR7 ASCSU
ID  _FAR7_ASCSU  STANDARD; PRT; 8 AA.
AC  F43171;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  01-FEB-1996 (Rel. 33, Last annotation update)
DE  FMRamide-like neuropeptide AF7.
OS  Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC  Ascarididae; Ascaris.
CX  NCBI_TaxID=6253;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=95380362; PubMed=7651904;
RA  Cowden C., Stretton A.O.W.;
RT  "Eight novel FMRamide-like neuropeptides isolated from the nematode
Ascaris suum.";
RL  Peptides 16:491-500(1995).
CC  -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
KW  Neuropeptide; Amidation.
FT  MOD_RES 8
SQ  SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match      27.9%; Score 12; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 PR 4
Db  3 PR 4

RESULT 9
LMT2 LOCM1
ID  _LMT2_LOCM1  STANDARD; PRT; 8 AA.
AC  P22396;
DT  01-AUG-1991 (Rel. 19, Created)
DT  01-AUG-1991 (Rel. 19, Last sequence update)
DT  01-AUG-1991 (Rel. 19, Last annotation update)
DE  Locustamyotropin 2 (LOM-MT-2).
OS  Locusta migratoria (Migratory locust).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC  Acridoidea; Acrididae; Oedipodinae; Locusta.
CX  NCBI_TaxID=7004;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Corpora cardiaca;
RA  Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT  "Isolation, identification and synthesis of locustamyotropin II, an

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RT additional neuropeptide of Locusta migratoria. Member of the
 RL cephalomyotropic peptide family.;
 RL Insect Biochem. 20:479-484(1990).

CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 CC activity).
 CC -!- SIMILARITY: Belongs to the pyrokinin family.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8
 FT MOD RES 8 AMIDATION.
 SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;

Query Match 27.9%; Score 12; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PR 4
 ||
 DB 6 PR 7

RESULT 10

LPK_LEUMA

ID LPK_LEUMA STANDARD; PRT; 8 AA.

AC P13049;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Leukopyrokinin (LPK) (LEM-PK).

OS Leucophaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

OC Blaberidae; Leucophaea.

OX NCBI_TaxID=62988;

RN [1]

RP SEQUENCE.

RX MEDLINE=86269041; PubMed=3015140;

RA Nachman R.J., Holman G.M., Cook B.J.;

RT "Active fragments and analogs of the insect neuropeptide

RT leucopyrokinin: structure-function studies.";

RL Biochem. Biophys. Res. Commun. 137:936-942(1986).

RN [2]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Head;

RX MEDLINE=87052651; PubMed=2877794;

RA Holman G.M., Cook B.J., Nachman R.J.;

RT "Primary structure and synthesis of a blocked myotropic

RT neuropeptide isolated from the cockroach, Leucophaea maderae.";

RL Comp. Biochem. Physiol. 85C:219-224(1986).

CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic

CC activity).

CC -!- MISCELLANEOUS: An analog without the N-terminal PCA residue was

CC synthesized and found to exhibit greater activity (144%) than the

CC parent neuropeptide. The portion of the sequence of LPK most

CC critical for the myotropic properties is limited to the

CC pentapeptide fragment FTPLR.

CC -!- SIMILARITY: Belongs to the pyrokinin family.

DR PR; A23967; A23967.

DR InterPro: IPR001484; Pyrokinin.

DR PROSITE: PS00539; PYROKININ; 1.

KW Neuropeptide; Amidation; Pyrokinin; Pyrokinin; Pyrokinin; Pyrokinin.

FT MOD RES 1 1 PYROLIDONE CARBOXYLIC ACID.

FT MOD RES 8 8 AMIDATION.

SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Query Match 27.9%; Score 12; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PR 4
 ||
 DB 6 PR 7

RESULT 11

PPK3_PERAM

ID PPK3_PERAM STANDARD; PRT; 8 AA.

AC P82618;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pyrokinin-3 (Pea-PK-3) (FXPLR-amide).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;

OC Blattidae; Periplaneta.

OX NCBI_TaxID=6978;

RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Retrocerebral complex;

RX MEDLINE=99212469; PubMed=10196736;

RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;

RT "Differential distribution of pyrokinin-isoforms in cerebral and

RT abdominal neurohemal organs of the American cockroach.";

RL Insect Biochem. Mol. Biol. 29:139-144(1999).

RN [2]

RP TISSUE SPECIFICITY.

RX MEDLINE=20189894; PubMed=10723010;

RA Predel R., Eckert M.;

RT "Tagma-specific distribution of FXPLR-amides in the nervous system of

RT the American cockroach.";

RL J. Comp. Neurol. 419:352-363(2000).

CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic

CC activity).

CC -!- TISSUE SPECIFICITY: Corpora cardiaca.

CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.

CC -!- SIMILARITY: Belongs to the Pyrokinin family.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD RES 8 8 AMIDATION.

SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 27.9%; Score 12; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PR 4
 ||
 DB 6 PR 7

RESULT 12

RS7_MYCIT

ID RS7_MYCIT STANDARD; PRT; 8 AA.

AC P33564;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 30S ribosomal protein S7 (Fragment).

GN RPSG.

OS Mycobacterium intracellulare.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1767;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93197130; PubMed=9451173;

RA Nair J., Rouse D.A., Morris S.L.;

RT "Nucleotide sequence analysis of the ribosomal S12 gene of

RT Mycobacterium intracellulare.";

RL Nucleic Acids Res. 21:1039-1039(1993).

CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds

CC directly to 16S rRNA where it nucleates assembly of the head

CC domain of the 30S subunit. Is located at the subunit interface

CC close to the decoding center, probably blocks exit of the E-site

CC tRNA (By similarity).

CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9


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CC and S11 (By similarity).
CC -!- SIMILARITY: Belongs to the S7P family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EVBL; L08171; AAA25376.1; -.
CC DR PIR; S35538; S35538.
CC DR HAVAP; MF 00480; -.
CC DR InterPro; IPR000235; Ribosomal S7.
CC DR PROSITE; PS00052; RIBOSOMAL S7; PARTIAL.
CC KW Ribosomal protein; RNA-binding; rRNA-binding; tRNA-binding.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC FT NON_TER 8 8
CC SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;
CC
CC Query Match 27.9%; Score 12; DB 1; Length 8;
CC Best Local Similarity 100.0%; Pred. No. 1.4e+05;
CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 3 PR 4
CC DB 1 PR 2
CC
CC RESULT 13
CC UC26_MAIZE STANDARD; PRT; 8 AA.
CC AC P80632;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
CC DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
CC (Fragment).
CC OS Zea mays (Maize).
CC CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC CC PACCAD clade; Panicoideae; Andropogoneae; Zea.
CC OX NCBI_TaxID=4577;
CC RN [1]
CC RP SEQUENCE.
CC RC TISSUE=Coleoptile;
CC RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
CC RA Pernollet J.-C., Zivy M., de Vienne D.;
CC RT "The maize two dimensional gel protein database: towards an integrated
CC RT genome analysis program.";
CC RL Theor. Appl. Genet. 93:997-1005(1996).
CC CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC CC protein is: 7.0, its MW is: 57.2 kDa.
CC DR Maize-2DPAGE; P80632; COLEOPTILE.
CC FT NON_TER 1 1
CC FT NON_TER 8 8
CC SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;
CC
CC Query Match 27.9%; Score 12; DB 1; Length 8;
CC Best Local Similarity 100.0%; Pred. No. 1.4e+05;
CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 3 PR 4
CC DB 3 PR 4
CC
CC RESULT 14
CC UPAL_HUMAN STANDARD; PRT; 8 AA.
CC ID UPAL_HUMAN
CC AC P30087;
CC DT 01-APR-1993 (Rel. 25, Created)

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DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE.
CC RC TISSUE=Plasma;
CC RX MEDLINE=93092937; PubMed=1459097;
CC RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
CC RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
CC RA Hochstrasser D.F.;
CC RL "Plasma protein map: an update by microsequencing.";
CC RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC CC protein is: 4.9, its MW is: 65 kDa.
CC DR SWISS-2DPAGE; P30087; HUMAN.
CC FT NON_TER 1 1
CC FT UNSURE 8 8
CC FT NON_TER 8 8
CC SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;
CC
CC Query Match 27.9%; Score 12; DB 1; Length 8;
CC Best Local Similarity 100.0%; Pred. No. 1.4e+05;
CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 3 PR 4
CC DB 7 PR 8
CC
CC RESULT 15
CC PSK_DAUCA STANDARD; PRT; 5 AA.
CC ID PSK_DAUCA
CC AC P58261;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Phytosulfokine-alpha (PSK-alpha) (Contains: Phytosulfokine-beta (PSK-
CC beta)).
CC OS Daucus carota (Carrot).
CC CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
CC CC Campanulids; Apiales; Apiaceae; Scandiceae; Daucinae;
CC CC Daucus.
CC OX NCBI_TaxID=4039;
CC RN [1]
CC RP SEQUENCES, AND IDENTIFICATION BY MASS SPECTROMETRY.
CC RX STRAIN=cv. US-Harumakigosun;
CC RX MEDLINE=20212743; PubMed=10750705;
CC RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
CC RA Kamada H., Sakagami Y.;
CC RA "A secreted peptide growth factor, phytosulfokine, acting as a
CC RT stimulatory factor of carrot somatic embryo formation.";
CC RL Plant Cell Physiol. 41:27-32(2000).
CC -!- FUNCTION: In presence of 2,4-D, stimulates proliferation of the
CC CC cells, but does not stimulate differentiation into the somatic
CC CC embryos
CC CC -!- SUBCELLULAR LOCATION: Secreted.
CC CC -!- PTM: Sulfation is important for activity and for the binding to a
CC CC putative membrane receptor (By similarity).
CC CC -!- SIMILARITY: Belongs to the phytosulfokine family.
CC KW Growth factor; Sulfation.
CC FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
CC FT MOD_RES 1 1 SULFATION.
CC FT MOD_RES 3 3 SULFATION.
CC SQ SEQUENCE 5 AA; 687 MW; 76C1B5B04B300000 CRC64;
CC
CC Query Match 25.6%; Score 11; DB 1; Length 5;
CC Best Local Similarity 100.0%; Pred. No. 1.4e+05;
CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 7 IV 8
||
Db 2 IV 3

Search completed: July 28, 2004, 07:54:11
Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:43:54 ; Search time 34 Seconds
(without alignments)
74.240 Million cell updates/sec

Title: SEQ3

Perfect score: 43

Sequence: 1 qprraaiy 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 489

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:

- 1: sp_archaea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mhc:
- 8: sp_organelle:
- 9: sp_phage:
- 10: sp_plant:
- 11: sp_rodent:
- 12: sp_virus:
- 13: sp Vertebrate:
- 14: sp Unclassified:
- 15: sp_rvirus:
- 16: sp_bacteriaph:
- 17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	37.2	7	8 P92214	P92214 amblyopyrum
2	16	37.2	7	8 P92393	P92393 hordeum vul
3	16	37.2	7	8 P92403	P92403 lophopyrum
4	16	37.2	7	8 P92427	P92427 peridictyon
5	16	37.2	7	8 P92430	P92430 aegilops ta
6	16	37.2	7	8 P92221	P92221 bromus iner
7	16	37.2	7	8 P92425	P92425 pseudoroegn
8	16	37.2	7	8 P92381	P92381 hordeum bra
9	16	37.2	7	8 P92387	P92387 henrardia p
10	16	37.2	7	8 P92210	P92210 agropyron c
11	16	37.2	7	8 P92440	P92440 thimopyrum
12	16	37.2	7	8 P92218	P92218 australopyr
13	16	37.2	7	8 P92390	P92390 heteranthel
14	16	37.2	7	8 P92372	P92372 haynaldia v
15	16	37.2	7	8 P92442	P92442 taenlatheru
16	16	37.2	7	8 P92226	P92226 crithopsis

17	16	37.2	7	8 P92385	P92385 hordeum mar
18	16	37.2	7	8 P92421	P92421 psathyrosta
19	16	37.2	8	11 Q9JLD7	Q9JLD7 mesocricetu
20	15	34.9	8	8 Q9GCZ4	Q9GCZ4 nenga pumil
21	15	34.9	8	8 Q9GD00	Q9GD00 masoala mad
22	15	34.9	8	8 Q9GD47	Q9GD47 hydriastele
23	14	32.6	8	12 Q9J205	Q9J205 hepatitis c
24	13	30.2	7	2 Q50556	Q50556 actinobacil
25	13	30.2	8	4 Q15900	Q15900 homo sapien
26	13	30.2	8	5 Q94623	Q94623 manduca sex
27	13	30.2	8	11 Q62528	Q62528 mus spretus
28	12	27.9	7	12 Q66113	Q66113 cherry leaf
29	12	27.9	8	2 Q56759	Q56759 xanthobacte
30	12	27.9	8	2 Q9RQ57	Q9RQ57 buchnera ap
31	12	27.9	8	4 Q81VK3	Q81VK3 homo sapien
32	12	27.9	8	6 Q9GMH3	Q9GMH3 lagenorhync
33	12	27.9	8	6 Q28866	Q28866 megaptera n
34	12	27.9	8	8 Q19961	Q19961 gossypium d
35	12	27.9	8	8 Q19958	Q19958 gossypium b
36	12	27.9	8	8 Q94V82	Q94V82 varanus yuw
37	12	27.9	8	8 Q19960	Q19960 gossypium m
38	12	27.9	8	8 Q19959	Q19959 gossypium t
39	12	27.9	8	8 Q19956	Q19956 gossypium a
40	12	27.9	8	10 Q8GTG5	Q8GTG5 lycopersico
41	11	25.6	7	5 Q7Z1C0	Q7Z1C0 caenorhabdi
42	11	25.6	7	15 Q8JEB1	Q8JEB1 human immun
43	11	25.6	8	2 Q9RQ43	Q9RQ43 buchnera ap
44	11	25.6	8	2 Q09258	Q09258 synchococc
45	11	25.6	8	2 Q9ZIE9	Q9ZIE9 neisseria m

ALIGNMENTS

RESULT 1

P92214 PRELIMINARY; PRT; 7 AA.
AC P92214;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein l1 (Fragment).
OS RPS11.
GN Amblyopyrum muticum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Amblyopyrum.
OX NCBI_TaxID=4595;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5572; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL EMBL; Z77756; CAB01346.1; --
DR Mol. Phylogenet. Evol. 7:217-230(1997).
DR GO; GO:0009507; C:chloroplast; IEA.
DR Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4

DB 1 PPK 3

RESULT 2

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P92393
ID P92393 PRELIMINARY; PRT; 7 AA.
AC P92393;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum vulgare (Barley).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H3139; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77764; CAB01370.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
DB 1 PPK 3

RESULT 3
P92403 PRELIMINARY; PRT; 7 AA.
ID P92403;
AC P92403;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Lophopyrum elongatum (Tall wheatgrass) (Aegilops elongatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Thinopyrum.
OX NCBI_TaxID=4588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6592; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77743; CAB01307.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
DB 1 PPK 3

P92403 PRELIMINARY; PRT; 7 AA.
ID P92403;
AC P92403;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6668; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77758; CAB01352.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
DB 1 PPK 3

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RESULT 4
P92427 PRELIMINARY; PRT; 7 AA.
ID P92427;
AC P92427;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Peridictyon sanctum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Peridictyon.
OX NCBI_TaxID=37683;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5575; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77749; CAB01325.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
DB 1 PPK 3

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RESULT 5
P92430 PRELIMINARY; PRT; 7 AA.
ID P92430;
AC P92430;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6668; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77758; CAB01352.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
DB 1 PPK 3

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Qy      2 PPR 4
Db      1 PPK 3

Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
P92221 ID P92221 PRELIMINARY; PRT; 7 AA.
AC P92221;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Bromus inermis (Smooth brome grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Bromus.
OX NCBI_TaxID=15371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OSA414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."; Evol. 7:217-230(1997).
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01355.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PPR 4
Db      1 PPK 3

Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
P92425 ID P92425 PRELIMINARY; PRT; 7 AA.
AC P92425;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Pseudoroegneria.
OX NCBI_TaxID=4604;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H9082; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."; Evol. 7:217-230(1997).
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77744; CAB01310.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;

Qy      2 PPR 4
Db      1 PPK 3

Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
P92381 ID P92381 PRELIMINARY; PRT; 7 AA.
AC P92381;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum brachyantherum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=52712;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."; Evol. 7:217-230(1997).
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77761; CAB01361.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PPR 4
Db      1 PPK 3

Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
P92387 ID P92387 PRELIMINARY; PRT; 7 AA.
AC P92387;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Henrardia persica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Henrardia.
OX NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data."; Evol. 7:217-230(1997).
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01322.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PPR 4
Db      1 PPK 3

Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;
Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
   ||:
   1 PPK 3

Db

RESULT 10
P92210
ID P92210 PRELIMINARY; PRT; 7 AA.
AC P92210;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Agropyron cristatum (Crested wheatgrass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4349; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
DR EMBL; Z77771; CAB01391.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
   ||:
   1 PPK 3

Db

RESULT 11
P92440
ID P92440 PRELIMINARY; PRT; 7 AA.
AC P92440;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Thinopyrum bessarabicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Thinopyrum.
OX NCBI_TaxID=4501;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6725; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
DR EMBL; Z77769; CAB01385.1; -.

SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;
Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
   ||:
   1 PPK 3

Db

RESULT 12
P92218
ID P92218 PRELIMINARY; PRT; 7 AA.
AC P92218;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Australopyrum retrofractum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Australopyrum.
OX NCBI_TaxID=4597;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6723; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230 (1997).
DR EMBL; Z77767; CAB01379.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPR 4
   ||:
   1 PPK 3

Db

RESULT 13
P92390
ID P92390 PRELIMINARY; PRT; 7 AA.
AC P92390;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Heteranthelium piliferum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Heteranthelium.
OX NCBI_TaxID=37679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5557; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";

```

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RT sequence data.";
RL Mol., Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77750; CAB01328.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR Chloroplast.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4
Db 1 PPK 3

RESULT 14
P92372 PRELIMINARY; PRT; 7 AA.
AC P92372
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DD 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Haynaldia villosa.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Haynaldia.
ON NCBI_TaxID=40247;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5561; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol., Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77741; CAB01301.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4
Db 1 PPK 3

RESULT 15
P92442 PRELIMINARY; PRT; 7 AA.
AC P92442
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DD 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Taeniatherum caput-medusae (Medusahead).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Taeniatherum.
ON NCBI_TaxID=37687;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H10254; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol., Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77741; CAB01301.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4
Db 1 PPK 3

MEDLINE=97271648; PubMed=9126564;
RX Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol., Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77760; CAB01358.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 37.2%; Score 16; DB 8; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PPR 4
Db 1 PPK 3

Search completed: July 28, 2004, 07:54:56
Job time : 35 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:15:39 ; Search time 50 seconds
(without alignments)
45.208 Million cell updates/sec

Title: SEQ3

Perfect score: 43

Sequence: 1 qppraaiy 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 122046

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	8	3 AAB19055	Aab19055 Amino aci
2	38	88.4	8	2 AAY28537	Aay28537 Beta-1 in
3	36	83.7	8	2 AAW06877	Aaw06877 Glycosami
4	33	76.7	7	2 AAY28538	Aay28538 Beta-1 in
5	31	72.1	8	2 AAR59381	Aar59381 Fibronect
6	31	72.1	8	2 AAR56244	Aar56244 Fibronect
7	31	72.1	8	2 AAY78582	Aay78582 Fibronect
8	31	72.1	8	2 AAR83682	Aar83682 33 kD fib
9	31	72.1	8	2 AAW46437	Aaw46437 Synthetic
10	31	72.1	8	2 AAW19843	Aaw19843 Chimeric
11	31	72.1	8	2 AAW73537	Aaw73537 Fibronect
12	31	72.1	8	2 AAW81843	Aaw81843 Fibronect
13	31	72.1	8	2 AAY32881	Aay32881 Fibronect
14	31	72.1	8	2 AAY32869	Aay32869 Fibronect
15	31	72.1	8	2 AAY28545	Aay28545 Beta-1 in
16	31	72.1	8	4 AAB91965	Aab91965 Fibronect
17	31	72.1	8	4 AAB91982	Aab91982 Fibronect
18	28	65.1	6	2 AAR62181	Aar62181 Ul snRNP
19	28	65.1	7	2 AAR73883	Aar73883 Rubella v
20	26	60.5	6	2 AAY28511	Aay28511 Beta-1 in
21	26	60.5	6	3 AAB19065	Aab19065 Amino aci
22	25	58.1	7	2 AAR73902	Aar73902 Streptoco
23	25	58.1	7	7 ADC44364	Adc44364 Endotheli
24	25	58.1	8	2 AAY40669	Aay40669 A2 deriva
25	25	58.1	8	3 AAB30008	Aab30008 Scaffold

26	24	55.8	7	2 AAR73879	Aar73879 Rubella v
27	24	55.8	7	4 AAG98209	Aag98209 Human SNP
28	23	53.5	7	2 AAR09404	Aar09404 LFA-1 alp
29	23	53.5	7	7 ADC28167	Adc28167 Synthetic
30	22	51.2	7	2 AAW34386	Aaw34386 PKB subst
31	22	51.2	7	2 AAW71730	Aaw71730 Peptide #
32	22	51.2	7	3 AAY95265	Aay95265 Crostide
33	22	51.2	7	4 AAB99790	Aab99790 Protein k
34	22	51.2	7	4 AAG65169	Aag65169 AKT inhib
35	22	51.2	7	4 AAB83202	Aab83202 PKA inhib
36	22	51.2	7	4 AAB59271	Aab59271 Phosphory
37	22	51.2	7	5 AAG66179	Aag66179 Peptide s
38	22	51.2	7	5 AAO19502	Aao19502 AKT inhib
39	22	51.2	7	6 ABU08523	Abu08523 Protein k
40	22	51.2	7	7 ADC81657	Adc81657 Protein k
41	22	51.2	7	7 ADE49662	Ade49662 Pyrazole
42	22	51.2	8	2 AAR32362	Aar32362 Sample pe
43	22	51.2	8	2 ABB76926	Abb76926 Cyclohex
44	22	51.2	8	2 AAY33180	Aay33180 Human pef
45	22	51.2	8	2 AAY48023	Aay48023 Immunogen

ALIGNMENTS

RESULT 1

AAB19055

ID AAB19055 standard; peptide; 8 AA.

XX

AC AAB19055;

XX

DT 08-FEB-2001 (first entry)

XX

DE Amino acid sequence of a betal-integrin inhibitor.

XX

KW Betal-integrin inhibitor; leukocyte mediated tissue destruction;

KW Central nervous system ischemic injury; myocardial infarction;

KW Betal-integrin; angioplasty; surgical incision; injury-related trauma;

KW Transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.

XX

OS Synthetic.

XX

PN WO2000056350-A2.

XX

PD 28-SEP-2000.

XX

PF 22-MAR-2000; 2000WO-US007680.

XX

PR 22-MAR-1999; 99US-0125634P.

XX

PR 24-NOV-1999; 99US-0167538P.

PA

(MINU) UNIV MINNESOTA.

PA (TEXA) UNIV TEXAS SYSTEM.

XX

XX (SENT-) SENTRON MEDICAL INC.

PI

PI McCarthy JB, Mileski WJ, Jamieson GA, Low WC, Sawchuk RJ;

PI Furcht LT;

DR WPI; 2000-656062/63.

XX

PT Inhibition of inflammatory leukocyte mediated destruction of tissue in a patient, comprises administering a peptide inhibitor of betal-integrin,

PT useful for treatment of e.g. cancer and osteoporosis.

XX

XX Claim 3; Page 38; 61pp; English.

PS

CC AAB19054-67 represent betal-integrin inhibitors. The peptides inhibit

CC betal-integrin which is responsible for leukocyte mediated tissue

CC destruction. The peptides are useful for inhibiting inflammatory

CC leukocyte mediated destruction of tissue which occurs as a result of

CC central nervous system (CNS) ischemic injury, myocardial infarction,

CC angioplasty, surgical incisions, injury-related trauma, and/or transplant

CC reperfusion, exposure to heat, cold, light, electricity and/or chemicals.

CC They are also useful for the treatment of stroke, a burn type injury,
 CC cancer, and osteoporosis

SQ Sequence 8 AA;

Query Match 100.0%; Score 43; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPPRAAIY 8
 |||||

DB 1 QPPRAAIY 8

RESULT 2

AAV28537
 ID AAV28537 standard; peptide; 8 AA.

XX AC AAV28537;

DT 19-OCT-1999 (first entry)

DE Beta-1 integrin cell adhesion modulator analogue #22.

XX Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;

KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.

XX OS Synthetic.

XX WO9937669-A1.

XX PD 29-JUL-1999.

XX 21-JAN-1999; 99WO-US001236.

XX 22-JAN-1998; 98US-00721119P.

XX 12-AUG-1998; 98US-0096211P.

XX 12-AUG-1998; 98US-0096212P.

XX PA (MINU) UNIV MINNESOTA.

XX PI McCarthy JB, Furcht LT, Brienza A;

XX DR WPI; 1999-469112/39.

XX New peptides modulating beta1 integrin subunit dependent cell adhesion,
 PT useful to study cell adhesion e.g. alpha4beta1 integrin dependent
 PT adhesion important in tumor cell biology.

XX Example 4; Fig 7; 47pp; English.

XX This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAV28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which has
 CC a side chain including an aromatic group, and a penultimate C-terminal
 CC amino acid residue (Lip) with an alkyl side chain group, i.e. a 'LipAr'
 CC motif. Studies with these peptides have also shown that inhibiting
 CC peptides do not contain D-amino acids and that it is the presence of the
 CC ArLip motif that conveys effective beta1 integrin dependent cell adhesion
 CC inhibition. The beta-1 integrin subunit dependent cell adhesion is
 CC important for cell adhesion to extracellular matrix proteins, and the
 CC subunit is expressed on tumours such as melanomas. Therefore these LipAr
 CC motif containing peptides may be important in the treatment of cancer

XX SQ Sequence 8 AA;

Query Match 88.4%; Score 38; DB 2; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAIY 8
 |||||

DB 1 QPPRAAIY 8

RESULT 3

AAW06877
 ID AAW06877 standard; peptide; 8 AA.

XX AC AAW06877;

DT 18-MAR-1997 (first entry)

XX Glycosaminoglycan binding peptide from fibronectin.

XX Complement inhibitor; membrane co-factor protein; MCP;
 KW decay accelerating factor; DAF; chimeric protein; glycosaminoglycan;
 KW heparin; cell lysis; sepsis; adult respiratory distress syndrome;
 KW reperfusion injury; cell damage; therapy; fibronectin.

XX OS Synthetic.

XX WO9634965-A2.

XX PD 07-NOV-1996.

XX 03-MAY-1996; 96WO-US006301.

XX 05-MAY-1995; 95US-00435149.

XX PA (CHIR) CHIRON CORP.

XX PI Innis MA, Zaror I, Creasey AA;

XX DR WPI; 1996-506167/50.

XX Chimeric proteins for inhibiting complement-mediated cell lysis -
 PT comprise membrane co-factor protein and decay accelerating factor peptide
 PT sequences.

XX Claim 9; Page 26; 33pp; English.

XX A glycosaminoglycan binding peptide (AAW06877) derived from fibronectin
 CC is utilised in novel chimeric proteins of the formula A-R1-B-R2-C, where
 CC A and C are peptides (AAW06875-79, AAW06883-90) capable of binding
 CC glycosaminoglycans (esp. heparin), present on cell surfaces. R1 is
 CC membrane co-factor protein (MCP) or decay accelerating factor (DAF), R2
 CC is DAF when R1 is MCP or MCP when R1 is DAF, and B is a peptide that may
 CC have complement inhibitor activity. The chimeric proteins (see also
 CC AAW06882) are directed to cell surfaces where they inhibit complement-
 CC mediated cell lysis. They are used to treat and prevent disease states in
 CC which complement plays a role, e.g. sepsis, adult respiratory distress
 CC syndrome, reperfusion injury and tissue damage

XX SQ Sequence 8 AA;

Query Match 83.7%; Score 36; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
 |||||

DB 2 QPPRAAI 8

RESULT 4

AAV28538
 ID AAV28538 standard; peptide; 7 AA.

XX AC AAV28538;

XX DT 19-OCT-1999 (first entry)

XX DE Beta-1 integrin cell adhesion modulator analogue #23.

KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
 KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX Synthetic.
 OS

PN WO9937669-A1.
 XX

XX 29-JUL-1999.
 PD

XX 21-JAN-1999; 99WO-US001236.
 XX

XX 22-JAN-1998; 98US-0072119P.
 PR

XX 12-AUG-1998; 98US-0096211P.
 PR

XX 12-AUG-1998; 98US-0096212P.
 PR

XX (MINU) UNIV MINNESOTA.
 PA

XX McCarthy JB, Furcht LT, Brienza A;
 PI

XX WPI; 1999-469112/39.
 DR

XX New peptides modulating betal integrin subunit dependent cell adhesion,
 XX

XX useful to study cell adhesion e.g. alpha4betal integrin dependent
 PT

XX adhesion important in tumor cell biology.
 PT

XX Example 4; Fig 7; 47pp; English.
 XX

XX This sequence is a C-terminal tyrosine tagged peptide. This peptide
 CC inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 CC AAV28510-Y28549 have been used to show that peptides which modulate this
 CC form of cell adhesion need a C-terminal amino acid residue (Ar) which has
 CC a side chain including an aromatic group, and a penultimate C-terminal
 CC amino acid residue (Lip) with an alkyl side chain group, i.e. a 'LipAr'
 CC motif. Studies with these peptides have also shown that inhibiting
 CC peptides do not contain D-amino acids and that it is the presence of the
 CC Arlip motif that conveys effective betal integrin dependent cell adhesion
 CC inhibition. The beta-1 integrin subunit dependent cell adhesion is
 CC important for cell adhesion to extracellular matrix proteins, and the
 CC subunit is expressed on tumours such as melanomas. Therefore these LipAr
 CC motif containing peptides may be important in the treatment of cancer
 XX

XX Sequence 7 AA;
 SQ

Query Match 76.7%; Score 33; DB 2; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX

Qy 2 PPRAAIY 8
 |||||

Db 1 PPRARIY 7
 |||||

RESULT 5

AAAR59381

ID AAR59381 standard; peptide; 8 AA.

AC AAR59381;

XX 25-MAR-2003 (revised)

DT 22-MAR-1995 (first entry)

XX Fibronectin fragment FN5.

XX Fibronectin; retro virus; HIV; AIDS; virucide; ovalbumin.

XX Synthetic.

XX WO9417097-A1.

XX 04-AUG-1994.

XX 19-JAN-1994; 94WO-US000729.

XX

PR 19-JAN-1993; 93US-00006121.
 XX (MINU) UNIV MINNESOTA.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wahl SM, McCarthy JB, Furcht LT;
 PI

XX WPI; 1994-264029/32.
 XX

XX New polypeptide comprising carrier molecule coupled to fibronectin
 PT fragment - useful in treatment of retroviral infections and associated
 PT diseases, e.g. AIDS.
 PT

XX Claim 1; Page 13; 18pp; English.
 PS

XX This peptide may be covalently linked to a carrier (especially
 CC ovalbumin). The resulting compound FN-C/H-V has excellent HIV virus
 CC inhibiting activity, low toxicity and high safety. It may be useful in
 CC the treatment of AIDS. (Updated on 25-MAR-2003 to correct PN field.)
 CC

XX Sequence 8 AA;
 SQ

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX

Qy 1 QPPRAAI 7
 |||||

Db 2 QPPRARI 8
 |||||

RESULT 6

AAAR56244

ID AAR56244 standard; peptide; 8 AA.

AC AAR56244;

XX 25-MAR-2003 (revised)

DT 12-JAN-1995 (first entry)

XX Fibronectin-derived peptide.

XX Fibronectin; inflammation; antiinflammatory; immunosuppressive;

XX leukocyte; arthritis; autoimmune disease; graft versus host disease.

XX Synthetic.

XX WO9413692-A1.

XX 23-JUN-1994.

XX 06-DEC-1993; 93WO-US011781.

XX 10-DEC-1992; 92US-00990296.

XX 21-OCT-1993; 93US-00139903.

XX (MINU) UNIV MINNESOTA.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Furcht JT, McCarthy JB, Wahl SM, Allen JB;
 PI

XX WPI; 1994-217799/26.
 DR

XX Fibronectin derived peptide(s) for treating inflammation - involving
 PT leukocyte activation, partic. arthritis and graft versus host disease.

XX Claim 8; Page 31; 45pp; English.
 PS

XX Chronic inflammation or autoimmune diseases are treated with peptides
 CC corresponding to residues 1906-24 (AAR56242), 1946-60 (AAR56243), 1892-99
 CC (AAR56244), 1961-85 (AAR56245), 1784-92 (AAR56246) and 1485-504
 CC (AAR56247) of fibronectin. (Updated on 25-MAR-2003 to correct PN field.)
 CC

XX

```

SQ      Sequence 8 AA;
Query Match      72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QPPRAAI 7
        |||||
DB      2 QPPRARI 8

RESULT 7
AAW78582
ID      AAW78582 standard; peptide; 8 AA.
XX
AC      AAW78582;
XX
DT      05-MAY-2000 (first entry)
XX
DE      Fibronectin derived peptide FN-C/H-V.
XX
KW      Fibronectin; intraocular fibroblast proliferation inhibitor; glaucoma;
KW      proliferative retinopathy; fibroblast migration; scarring.
XX
OS      Unidentified.
XX
PN      US6013628-A.
XX
PD      11-JAN-2000.
XX
PF      27-FEB-1995; 95US-00394748.
XX
PR      28-FEB-1994; 94US-00203458.
XX
PA      (MINU ) UNIV MINNESOTA.
XX
PI      Gregerson DS, Agarwal A, Wright MM, Murali S, Skubitz APN;
PI      Furcht LT, Balles M;
XX
DR      WPI; 1995-320291/41.
XX
PT      Treating proliferative vitreo:retinopathy, retinal scarring and glaucoma
PT      - using peptide derived from fibronectin, laminin or collagen.
XX
PS      Example 1; Col 15; 44pp; English.
XX
CC      This sequence represents a fibronectin derived peptide. Ocular
CC      administration of the peptide inhibits fibroblast proliferation and can
CC      be used in the treatment of glaucoma. The peptide can be used to treat
CC      proliferative vitreo:retinopathy by ocular administration of the peptides
CC      of the invention, which suppress fibroblast-mediated collagen gel
CC      contraction. The peptides can be used for treating glaucoma in mammals,
CC      especially humans, by inhibiting intraocular fibroblast proliferation,
CC      fibroblast migration and scarring
XX
SQ      Sequence 8 AA;
Query Match      72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QPPRAAI 7
        |||||
DB      2 QPPRARI 8

RESULT 8
AAR83682
ID      AAR83682 standard; peptide; 8 AA.
XX
AC      AAR83682;
XX
DT      25-MAR-2003 (revised)
XX
DE      Synthetic peptide Fn5 which binds pneumococci.
XX
KW      fibronectin; adherence; vaccine; antibody passive immunisation;
KW      diagnosis; screening; treatment; prevention; bacterial infection.
XX
OS      Synthetic.
XX
PN      WO9741151-A2.
XX
PD      06-NOV-1997.
XX
PF      01-MAY-1997; 97WO-US007198.
XX
PR      01-MAY-1996; 96US-0016632P.
XX
DT      11-APR-1996 (first entry)
XX
DE      33 KD fibronectin A chain peptide FN-C/H-V (1892-1899).
XX
KW      33 KD fragment; A chain; fibronectin; fibroblast; cell; proliferation;
KW      supression; epithelial; glial; epiretinal; eye; membranes; contraction;
KW      migration; vitreo:retinopathy; scarring; vitreo:retinal; glaucoma.
XX
OS      Synthetic.
XX
PN      WO9522979-A1.
XX
PD      31-AUG-1995.
XX
PF      28-FEB-1995; 95WO-US002478.
XX
PR      28-FEB-1994; 94US-00203458.
XX
PA      (MINU ) UNIV MINNESOTA.
XX
PI      Skubitz AP, Furcht LT, Balles M, Gregerson DS, Agarwal A;
PI      Wright MM, Murali S;
XX
DR      WPI; 1995-320291/41.
XX
PT      Treating proliferative vitreo:retinopathy, retinal scarring and glaucoma
PT      - using peptide derived from fibronectin, laminin or collagen.
XX
PS      Example 1; Page 29; 84pp; English.
XX
CC      A polypeptide which includes at least five amino acids from a fragment of
CC      the fibronectin A chain (AAR83679-84), C-terminal G domain of the laminin
CC      A chain (AAR83642/78) or NC1 domain of the alpha-2 chain of type IV
CC      collagen (AAR83639-41) suppresses fibroblast, epithelial and glial cell
CC      proliferation, contraction of epiretinal membranes and cell migration
CC      within the eye. It may be used in the treatment of proliferative
CC      vitreo:retinopathy, vitreo:retinal scarring and glaucoma. (Updated on 25-
CC      MAR-2003 to correct PR field.)
XX
SQ      Sequence 8 AA;
Query Match      72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QPPRAAI 7
        |||||
DB      2 QPPRARI 8

RESULT 9
AAW46437
ID      AAW46437 standard; peptide; 8 AA.
XX
AC      AAW46437;
XX
DT      14-MAY-1998 (first entry)
XX
DE      Synthetic peptide Fn5 which binds pneumococci.
XX
KW      fibronectin; adherence; vaccine; antibody passive immunisation;
KW      diagnosis; screening; treatment; prevention; bacterial infection.
XX
OS      Synthetic.
XX
PN      WO9741151-A2.
XX
PD      06-NOV-1997.
XX
PF      01-MAY-1997; 97WO-US007198.
XX
PR      01-MAY-1996; 96US-0016632P.
XX

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PR 01-MAY-1996; 96US-00642250.
XX (UTRQ ) UNIV ROCKEFELLER.
PA Masure HR, Rosenow CI, Tucmanen E, Wizeman TM;
PI WPI; 1997-549682/50.
XX
XX New isolated streptococcal choline binding proteins - used to develop
PT products for treating or preventing bacterial infection and for
PT detection, diagnosis and screening.
XX
XX Claim 34; Page 14; 142pp; English.
XX
CC The present sequence represents a synthetic peptide, Fn5. Streptococcus
CC pneumoniae (pneumococci) adheres to fibronectin at a site within the
CC carboxy-terminal heparin II binding domain. An eight amino acid stretch
CC within the type III #14 repeat supports adherence. The present peptide is
CC based on these amino acids. S. pneumoniae binds directly to this peptide.
CC An antibody to Fn5 inhibits adherence of S. pneumoniae to whole
CC fibronectin by greater than 70%. The peptide can be used to prepare
CC vaccines. The antibodies can be used for passive immunisation,
CC diagnostics, or screening. The peptide can also be used for treating or
CC preventing bacterial infection
XX
XX Sequence 8 AA;
XX
XX Query Match 72.1%; Score 31; DB 2; Length 8;
XX Best Local Similarity 85.7%; Pred. No. 1.4e+06;
XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 QPPRAAI 7
Db 2 QPPRAI 8
XX
XX RESULT 11
XX AAW73537
XX ID AAW73537 standard; peptide; 8 AA.
XX AC AAW73537;
XX DT 04-MAR-1999 (first entry)
XX DE Fibronectin fragment, peptide FN-C/H-V.
XX XW Adhesion promoter; extra-cellular matrix peptide;
XX XW biomolecule immobilisation; fibronectin.
XX OS Synthetic.
XX PN US5853744-A.
XX PD 29-DEC-1998.
XX PF 20-AUG-1996; 96US-00699965.
XX PR 20-AUG-1996; 96US-00699965.
XX PA (MINU ) UNIV MINNESOTA.
XX PI Mooradian DL, Fields GB;
XX DR WPI; 1999-094819/08.
XX
XX Solid-phase method for modifying substrate with peptide, especially
XX adhesion-promoting peptide - applied to medical devices, e.g. vascular
XX grafts, uses peptide modified by photoreactive group for covalent
XX attachment.
XX
XX Claim 4; Fig 1; 14pp; English.
XX
XX This sequence represents a fragment of fibronectin, and is designated
XX peptide FN-C/H-V. This sequence is an adhesion promoting extra-cellular
XX matrix peptide, and can be used in the method of the invention. The
XX method is a solid-phase method for modifying a substrate surface to
XX include a biomolecule (I), and comprises: (a) providing an immobilised
XX (I), comprising a peptide having: (i) an N alpha-terminus; or (ii) an
XX active site, by covalently attaching it to a support; (b) attaching a
XX photoreactive crosslinking agent (II), having at least one photoreactive
XX group, to the immobilised peptide, in (i) at the N alpha-terminus or in
XX (ii) to the peptide at an amino acid that does not form part of the
XX active site; (c) removing the photoreactive analogue (Ia) of (I) from the
XX support; and (d) attaching (Ia) to a solid surface by activating the

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CC photoreactive group. The method is particularly used to immobilise (I) on
 CC medical devices, specifically adhesion-promoting peptides on vascular
 CC grafts such that adhesion of cells to the device is improved. More
 CC generally a wide range of peptides can be deposited on blood oxygenators,
 CC pumps or sensors; tubing; stents; pacemaker leads; heart valves; (I)
 CC catheters; artificial organs; or body implants generally. Bound (I)
 CC retains its native activity, specifically promotion of adhesion and
 CC spreading of vascular endothelial cells. The method ensures that (II)
 CC reacts with alpha-amino groups only (contrast use of soluble peptide
 CC where reaction may occur at epsilon-amino groups in the active site) and
 CC a large excess of (II) can be used to avoid wasting peptide
 XX
 XX

XX Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
 |||||
 Db 2 QPPRARI 8

RESULT 12

ID AAW81843 standard; peptide; 8 AA.

XX AAW81843;

XX 17-OCT-2003 (revised)
 DT 05-FEB-1999 (first entry)

XX Fibronectin-like peptide V.

XX Fibronectin; ischemia; treatment; inflammatory disease; A chain;
 KW heparin-binding; RGDS-mediated cell adhesion region.
 XX unidentified.

XX US5840691-A.
 PN 24-NOV-1998.

XX 07-JUN-1995; 95US-00480133.
 XX 10-DEC-1992; 92US-00990296.
 PR 21-OCT-1993; 93US-00139903.

XX (FURC/) FURCHT L T.
 PA (WAHL/) WAHL S M.
 PA (ALLE/) ALLEN J B.
 PA (BILL/) BILLUPS K L.
 PA (MCCA/) MCCARTHY J B.
 PA (EVER/) EVERETT J E.

XX Allen JB, Wahl SM, Everett JE, McCarthy JB, Furcht LT;
 PI Billups KL;
 PI WPI; 1999-034077/03.

XX Treatment of ischaemia - with fibronectin peptides.

XX Claim 1; Col 25-26; 35pp; English.

XX AAW81841-W81846 are peptides used in a method for treating ischemia using
 CC polypeptides with fibronectin activity. The method can be used for
 CC treating a number of disease such as those associated with inflammatory
 CC diseases by administering an effective amount of a composition containing
 CC a polypeptide having a sequence of at least 3 amino acids corresponding
 CC substantially to an amino acid sequence within the 33 kd carboxyl
 CC terminal heparin-binding region located on the A chain of fibronectin or
 CC an RGDS-containing amino acid sequence within the 11.5 kd RGDS-mediated
 CC cell adhesion region located on all isoforms of fibronectin. (Updated on

CC 17-OCT-2003 to standardise OS field)
 XX Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
 |||||
 Db 2 QPPRARI 8

RESULT 13

ID AAY32881 standard; peptide; 8 AA.

XX AAY32881;

XX 02-NOV-1999 (first entry)

XX Fibronectin protein heparin II binding domain peptide H-V.

XX Fibronectin; extracellular matrix. open wound healing; IIICS domain;
 KW acute gaping cutaneous wound; chronic cutaneous ulcer; therapy;
 KW wound healing promoter; cell binding domain; heparin II binding domain.
 XX Homo sapiens.

XX WO9942117-A1.

XX 26-AUG-1999.

XX 10-FEB-1999; 99WO-US002872.
 XX 18-FEB-1999; 98US-00025622.

XX (UYNV) UNIV NEW YORK STATE RES FOUND.
 XX Clark RA, Greiling D;
 PI WPI; 1999-527415/44.

XX New extracellular matrix used to accelerate healing of acute gaping
 PT cutaneous wounds and chronic cutaneous ulcers.
 XX Claim 14; Page 19; 43pp; English.

XX This sequence represents a fibronectin protein fragment used in the
 CC extracellular matrix of the invention. The extracellular matrix comprises
 CC two or more fibronectin domains in a backbone matrix, and is used to
 CC enhance wound healing. The fibronectin domain peptides used are
 CC preferably from the IIICS domain, the cell binding domain, or the heparin
 CC II binding domain of human fibronectin. The matrix facilitates wound
 CC healing by providing an environment that intrinsically recruits new
 CC tissue cells to the wound site. The new matrix is useful for facilitating
 CC wound healing, especially useful for treating open wounds such as acute
 CC gaping cutaneous wounds and chronic cutaneous ulcers. The problem of
 CC chronic, non-healing wounds is severe. These open wounds require long-
 CC term care and procedures that are costly and labour intensive.
 CC Furthermore, these wounds have a severe impact on the patients' quality of
 CC life. Prior compositions and matrices have not been useful or cost
 CC effective. The present invention provides a matrix for wound healing that
 CC meets these requirements, and overcomes the deficiencies of the prior
 CC matrices

XX Sequence 8 AA;

Query Match 72.1%; Score 31; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7

```

Db      2 QPPRAI 8
|||||
RESULT 14
AAY32869
ID AAY32869 standard; peptide; 8 AA.
XX
AC AAY32869;
XX
DT 02-NOV-1999 (first entry)
XX
DE Fibronectin protein heparin II binding domain peptide H-V.
XX
KW Fibronectin; extracellular matrix; wound healing promoter; IIICS domain;
KW cell binding domain; heparin II binding domain; haemostasis; therapy;
KW surgical incisional wound; traumatic wound; radiation wound;
KW cancer extirpation; venous leg ulcer; diabetic ulcer; pressure ulcer.
XX
OS Homo sapiens.
XX
PN WO9942126-A1.
XX
PD 26-AUG-1999.
XX
PF 10-FEB-1999; 99WO-US002873.
XX
PR 18-FEB-1998; 98US-00025706.
XX
PA (UNYNY ) UNIV NEW YORK STATE RES FOUND.
XX
PI Clark RA, Greiling D, Gaillit J;
XX
DR WPI; 1999-527421/44.
XX
PT Extracellular matrix for promoting wound healing containing recombinant
PT fibronectin-derived peptide and backbone matrix.
XX
PS Claim 14; Page 21; 48pp; English.
XX
CC This sequence represents a fibronectin protein fragment used in the
CC extracellular matrix (A) of the invention. (A) is used for promoting
CC wound healing, and comprises a recombinant fibronectin peptide,
CC containing peptide fragments from at least two fibronectin domains, and a
CC backbone matrix. The fibronectin domain peptides used are preferably from
CC the IIICS domain, the cell binding domain, or the heparin II binding
CC domain of human fibronectin. (A) provides haemostasis and an environment
CC that recruits new tissue cells to the site of the wound. (A) is used to
CC promote healing of acute or chronic wounds, e.g. surgical incisional
CC wounds, traumatic wounds, radiation wounds, cancer extirpations, venous
CC leg ulcers, diabetic ulcers and pressure ulcers
XX
SQ Sequence 8 AA;
Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRAI 8
|||||

RESULT 15
AAY28545
ID AAY28545 standard; peptide; 8 AA.
XX
AC AAY28545;
XX
DT 19-OCT-1999 (first entry)
XX
DE Beta-1 integrin cell adhesion modulator analogue #37.
XX

```

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KW Beta 1 integrin dependent cell adhesion; LipAr motif; tumour;
KW C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
XX
OS Synthetic.
XX
PN WO9937669-A1.
XX
PD 29-JUL-1999.
XX
PF 21-JAN-1999; 99WO-US001236.
XX
PR 22-JAN-1998; 98US-0072119P.
PR 12-AUG-1998; 98US-0096211P.
PR 12-AUG-1998; 98US-0096212P.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI McCarthy JB, Furcht LT, Brienza A;
XX
DR WPI; 1999-469112/39.
XX
PT New peptides modulating betal integrin subunit dependent cell adhesion,
PT useful to study cell adhesion e.g. alpha4betal integrin dependent
PT adhesion important in tumor cell biology.
XX
PS Example 8; Fig 13; 47pp; English.
XX
CC This peptide is used with AAY28510-Y28549 to show that peptides which
CC modulate beta-1 integrin subunit dependent cell adhesion need a C-
CC terminal amino acid residue (Ar) which has a side chain including an
CC aromatic group. They also need a penultimate C-terminal amino acid
CC residue (Lip) with an alkyl side chain group, i.e. a 'LipAr' motif.
CC Studies with these peptides have also shown that inhibiting peptides do
CC not contain D-amino acids and that it is the presence of the ArLip motif
CC that conveys effective betal integrin dependent cell adhesion inhibition.
CC The beta-1 integrin subunit dependent cell adhesion is important for cell
CC adhesion to extracellular matrix proteins, and the subunit is expressed
CC on tumours such as melanomas. Therefore these LipAr motif containing
CC peptides may be important in the treatment of cancer
XX
SQ Sequence 8 AA;
Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRAI 8
|||||

Search completed: July 28, 2004, 07:53:48
Job time : 52 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:55:00 ; Search time 41 Seconds
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Title: SEQ3

Perfect score: 43
Sequence: 1 qprraiy 8

Scoring table: BLOSUM62

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Searched: 1291235 seqs, 313682936 residues

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Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	72.1	8	9	US-09-765-614B-6
2	31	72.1	8	9	US-09-925-715-2
3	31	72.1	8	10	US-09-999-724-58
4	31	72.1	8	10	US-09-829-382-11
5	31	72.1	8	14	US-10-017-193-4
6	31	72.1	8	16	US-10-722-075-6
7	28	65.1	8	9	US-09-765-614B-3
8	28	65.1	8	16	US-10-722-075-3
9	25	58.1	7	14	US-10-286-457-92
10	24	55.8	7	16	US-10-346-737A-6
11	23	53.5	7	10	US-09-954-385-360
12	23	53.5	7	14	US-10-021-660-90
13	22	51.2	7	9	US-09-845-667-6
14	22	51.2	7	9	US-09-845-667-21
15	22	51.2	7	9	US-09-845-667-56

16	22	51.2	7	14	US-10-190-012-9	Sequence 9, Appli
17	22	51.2	7	14	US-10-148-786A-15	Sequence 15, Appli
18	22	51.2	8	9	US-09-245-764-4	Sequence 4, Appli
19	22	51.2	8	12	US-10-687-109-4	Sequence 4, Appli
20	21	48.8	7	9	US-09-845-667-13	Sequence 13, Appli
21	21	48.8	7	10	US-09-931-325A-120	Sequence 120, App
22	21	48.8	7	10	US-09-931-325A-124	Sequence 124, App
23	21	48.8	7	10	US-09-954-385-414	Sequence 414, App
24	21	48.8	7	10	US-09-930-915A-160	Sequence 160, App
25	21	48.8	7	10	US-09-930-915A-165	Sequence 165, App
26	21	48.8	8	8	US-08-344-824-263	Sequence 263, App
27	21	48.8	8	9	US-09-839-666-6	Sequence 6, Appli
28	21	48.8	8	10	US-09-931-325A-122	Sequence 122, App
29	21	48.8	8	10	US-09-930-915A-163	Sequence 163, App
30	21	48.8	8	12	US-10-372-735-65	Sequence 65, Appli
31	21	48.8	8	12	US-10-029-926B-14	Sequence 14, Appli
32	21	48.8	8	14	US-10-234-579-6	Sequence 6, Appli
33	21	48.8	8	15	US-10-032-037B-14	Sequence 14, Appli
34	21	48.8	8	15	US-10-029-988B-14	Sequence 14, Appli
35	21	48.8	8	15	US-10-032-423A-14	Sequence 14, Appli
36	20	46.5	4	9	US-09-802-077-59	Sequence 59, Appli
37	20	46.5	4	9	US-09-802-096-59	Sequence 59, Appli
38	20	46.5	4	9	US-09-871-974-12	Sequence 12, Appli
39	20	46.5	4	10	US-09-925-179-59	Sequence 59, Appli
40	20	46.5	4	15	US-10-137-867-186	Sequence 186, App
41	20	46.5	5	9	US-09-871-974-2	Sequence 2, Appli
42	20	46.5	5	16	US-10-716-293-115	Sequence 115, App
43	20	46.5	6	9	US-09-871-974-5	Sequence 5, Appli
44	20	46.5	7	9	US-09-845-667-2	Sequence 2, Appli
45	20	46.5	7	9	US-09-871-974-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-765-614B-6
; Sequence 6, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-09-765-614B-6

Query Match 72.1%; Score 31; DB 9; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPRAAI 7
DB 2 QPRAAI 8

RESULT 2
US-09-925-715-2
; Sequence 2, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:

```
; APPLICANT: Nymed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; FILE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fibronectin
; OTHER INFORMATION: peptide
US-09-925-715-2

Query Match          72.1%; Score 31; DB 9; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

RESULT 3
US-09-999-724-58
; Sequence 58, Application US/09999724
; Publication No. US20030022355A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
; FILE REFERENCE: 212960
; CURRENT APPLICATION NUMBER: US/09/999,724
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/101,751
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-999-724-58

Query Match          72.1%; Score 31; DB 10; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

RESULT 4
US-09-829-382-11
; Sequence 11, Application US/09829382
; Publication No. US20030175293A1
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; OTHER INFORMATION: attachment peptide from fibronectin
```

```
; Rosenow, Carsten I.
; Tuomanen, Elaine
; Wizenann, Theresa M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,382
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/847,065
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-158 ..
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-829-382-11

Query Match          72.1%; Score 31; DB 10; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

RESULT 5
US-10-017-193-4
; Sequence 4, Application US/10017193
; Publication No. US20030113478A1
; GENERAL INFORMATION:
; APPLICANT: Dang, Mai Huong
; APPLICANT: Chiu, Phillip
; TITLE OF INVENTION: Surface Coating Method and Coated Device
; FILE REFERENCE: 52200-8010
; CURRENT APPLICATION NUMBER: US/10/017,193
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attachment peptide from fibronectin
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US-10-017-193-4

Query Match 72.1%; Score 31; DB 14; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
:|||||
Db 2 EPPRAI 8

RESULT 6
US-10-722-075-6
; Sequence 6, Application US/10722075
; Publication No. US20040141922A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/10/722,075
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/08/960,054A
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-10-722-075-6

Query Match 72.1%; Score 31; DB 16; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
:|||||
Db 2 QPPRAI 8

RESULT 7
US-09-765-614B-3
; Sequence 3, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Heparin-binding
; OTHER INFORMATION: peptide
US-09-765-614B-3

Query Match 65.1%; Score 28; DB 9; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
:|||||
Db 2 EPPRAI 8

RESULT 8
US-10-722-075-3
; Sequence 3, Application US/10722075
; Publication No. US20040141922A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/10/722,075
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/08/960,054A
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Heparin-binding
; OTHER INFORMATION: peptide
US-10-722-075-3

Query Match 65.1%; Score 28; DB 16; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
:|||||
Db 2 EPPRAI 8

RESULT 9
US-10-286-457-92
; Sequence 92, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, base
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-92

Query Match 58.1%; Score 25; DB 14; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPPRA 5
:|||||
Db 1 QPPRS 5

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; APPLICANT: BOS Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; GENERAL INFORMATION:
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/10/021,660
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nuclear target motif
US-10-021-660-90

Query Match 53.5%; Score 23; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPRA 5
Db 1 PPRA 4

RESULT 13
US-09-845-667-6
; Sequence 6, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Philip
; Cross, Darren
; Alessi, Dario
; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Braman & Rogalsky], LLP
; STREET: P.O. Box 352
; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14424-0352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/845,667
; FILING DATE: 30-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/091,763
; FILING DATE: 19-JUN-1998
; APPLICATION NUMBER: PCT/GB96/03186
; FILING DATE: 20-DEC-1996
; APPLICATION NUMBER: GB 9526083.2
; FILING DATE: 20-DEC-1995
; APPLICATION NUMBER: GB 9610272.8
; FILING DATE: 16-MAY-1996
; APPLICATION NUMBER: GB 9615066.9
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 002.00041
; TELECOMMUNICATION INFORMATION:

; APPLICANT: St. Hilaire, Phaedria
; TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS
; FILE REFERENCE: 11225.16US01
; CURRENT APPLICATION NUMBER: US/10/346,737A
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Spacer
US-10-346-737A-6

Query Match 55.8%; Score 24; DB 16; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPPRA 5
Db 3 RPPRA 7

RESULT 11
US-09-954-385-360
; Sequence 360, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 360
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-360

Query Match 53.5%; Score 23; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PPRA 5
Db 4 PPRA 7

RESULT 12
US-10-021-660-90
; Sequence 90, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.

```

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/
/ TELEPHONE: 716-393-3002
/ TELEFAX: 716-393-3001
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-845-667-6

Query Match      51.2%; Score 22; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 PRAAIY 8
Db      2 PRAATF 7

RESULT 14
US-09-845-667-21
; Sequence 21, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Philip
;               Alessi, Dario
;               Cross, Darren
; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
;
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bramer & Rogalskyj, LLP
; STREET: P.O. Box 352
; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14424-0352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/845,667
; FILING DATE: 30-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/091,763
; FILING DATE: 19-JUN-1998
; APPLICATION NUMBER: PCT/GB96/03186
; FILING DATE: 20-DEC-1996
; APPLICATION NUMBER: GB 9526083.2
; FILING DATE: 20-DEC-1995
; APPLICATION NUMBER: GB 9610272.8
; FILING DATE: 16-MAY-1996
; APPLICATION NUMBER: GB 9615066.9
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bramer, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 002.00041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-393-3002
; TELEFAX: 716-393-3001
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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/ SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-845-667-21

Query Match      51.2%; Score 22; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 PRAAIY 8
Db      2 PRAATF 7

RESULT 15
US-09-845-667-56
; Sequence 55, Application US/09845667
; Patent No. US20020065221A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Philip
;               Alessi, Dario
;               Cross, Darren
; TITLE OF INVENTION: CONTROL OF PROTEIN SYNTHESIS, AND SCREENING METHOD
;
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bramer & Rogalskyj, LLP
; STREET: P.O. Box 352
; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14424-0352
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/845,667
; FILING DATE: 30-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/091,763
; FILING DATE: 19-JUN-1998
; APPLICATION NUMBER: PCT/GB96/03186
; FILING DATE: 20-DEC-1996
; APPLICATION NUMBER: GB 9526083.2
; FILING DATE: 20-DEC-1995
; APPLICATION NUMBER: GB 9610272.8
; FILING DATE: 16-MAY-1996
; APPLICATION NUMBER: GB 9615066.9
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bramer, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 002.00041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-393-3002
; TELEFAX: 716-393-3001
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-845-667-56

Query Match      51.2%; Score 22; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 PRAAIY 8
Db      2 PRAATF 7
/
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Wed Jul 28 09:31:26 2004

seq3.closed.rapb

Page 6

Db 2 PRAATF 7

Search completed: July 28, 2004, 08:00:13
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 07:52:54 ; Search time 18 Seconds
(without alignments)
22.945 Million cell updates/sec

Title: SEQ3

Perfect score: 43

Sequence: 1 qprraay 8

Scoring table: BLOSUM62

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 71086

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	72.1	8	1	US-08-291-349A-5
2	31	72.1	8	1	US-07-980-296-3
3	31	72.1	8	2	US-08-480-133A-3
4	31	72.1	8	2	US-08-699-965-2
5	31	72.1	8	2	US-08-435-149-6
6	31	72.1	8	2	US-09-025-706-10
7	31	72.1	8	3	US-08-394-748A-13
8	31	72.1	8	3	US-08-916-913A-3
9	31	72.1	8	3	US-09-025-822-10
10	31	72.1	8	3	US-08-847-065-11
11	31	72.1	8	3	US-08-960-054A-6
12	31	72.1	8	3	US-08-958-993A-6
13	31	72.1	8	4	US-08-959-206A-2
14	31	72.1	8	4	US-09-101-751A-58
15	31	72.1	8	4	US-09-591-564-3
16	31	72.1	8	4	US-09-925-715-2
17	31	72.1	8	5	PCT-US93-11781-3
18	31	72.1	8	5	PCT-US95-03478-13
19	28	65.1	6	1	US-08-704-170-89
20	28	65.1	6	5	PCT-US94-02631-89
21	28	65.1	7	1	US-08-127-499A-7
22	28	65.1	7	1	US-08-482-847-7
23	28	65.1	8	3	US-08-960-054A-3
24	28	65.1	8	3	US-08-958-993A-3
25	25	58.1	7	1	US-08-127-499A-25
26	25	58.1	7	1	US-08-482-847-25
27	24	55.8	7	1	US-08-127-499A-3

28 55.8 7 1 US-08-482-847-3 Sequence 3, Appli
29 51.2 8 4 US-09-245-764-4 Sequence 4, Appli
30 21 48.8 6 1 US-08-127-499A-22 Sequence 22, Appli
31 21 48.8 6 1 US-08-482-847-22 Sequence 22, Appli
32 21 48.8 7 2 US-08-769-745-33 Sequence 33, Appli
33 21 48.8 8 2 US-08-737-085A-6 Sequence 6, Appli
34 21 48.8 8 3 US-09-246-258-6 Sequence 6, Appli
35 21 48.8 8 3 US-09-532-106-6 Sequence 6, Appli
36 21 48.8 8 4 US-09-839-666-6 Sequence 6, Appli
37 20 46.5 4 1 US-08-171-737-3 Sequence 3, Appli
38 20 46.5 4 1 US-08-202-178-9 Sequence 9, Appli
39 20 46.5 4 1 US-08-713-484-9 Sequence 9, Appli
40 20 46.5 4 2 US-08-955-263-9 Sequence 9, Appli
41 20 46.5 4 2 US-08-232-539D-46 Sequence 46, Appli
42 20 46.5 4 3 US-08-466-151-59 Sequence 59, Appli
43 20 46.5 4 4 US-08-466-163B-59 Sequence 59, Appli
44 20 46.5 4 4 US-09-802-096-59 Sequence 59, Appli
45 20 46.5 5 1 US-08-171-737-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-291-349A-5
; Sequence 5, Application US/08291349A
; Patent No. 5545620
; GENERAL INFORMATION:
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; TITLE OF INVENTION: Synthetic Fibronectin Fragments As
; TITLE OF INVENTION: Inhibitors of Retroviral Infection
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,349A
; FILING DATE: 16 AUG 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006,121
; FILING DATE: 19 JAN 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,673-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "FN5 (1892-1899)

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; OTHER INFORMATION: fibronectin fragment : FN-C/H-V"
US-08-291-349A-5
Query Match 72.1%; Score 31; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRARI 8

RESULT 2
US-07-990-296-3
; Sequence 3, Application US/07990296
; Patent No. 5591719
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: McCarthy, James B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: Allen, Janice B.
; TITLE OF INVENTION: Method for Treating Acute and
; TITLE OF INVENTION: Chronic Inflammatory Disorders Using Polypeptides
; TITLE OF INVENTION: with Fibronectin Activity
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5591719west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/990,296
; FILING DATE: 19921210
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Alan W.
; REGISTRATION NUMBER: 31,535
; REFERENCE/DOCKET NUMBER: 600.252-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal Fragment
; ORIGINAL SOURCE: Synthetically Derived
; FEATURE:
; NAME/KEY: Fragment of the 33 kD carboxy
; NAME/KEY: terminal heparin-binding fragment of the A
; NAME/KEY: chain of fibronectin
; LOCATION: Represents isolated fibronectin
; LOCATION: residues 1892-1899 from all plasma isoforms
; LOCATION: of fibronectin
US-07-990-296-3
Query Match 72.1%; Score 31; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRARI 8

RESULT 3
US-08-480-133A-3
; Sequence 3, Application US/08480133A
; Patent No. 5840691
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: McCarthy, James B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: Allen, Janice B.
; APPLICANT: Billups, Kevin L.
; APPLICANT: Everett, Jeffrey B.
; TITLE OF INVENTION: Method for Treating Inflammatory
; TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5840691west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,133A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,903
; FILING DATE: 21-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,296
; FILING DATE: 10-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 600-308US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-480-133A-3
Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRARI 8

RESULT 4
US-08-699-965-2
; Sequence 2, Application US/08699965
; Patent No. 5853744
; GENERAL INFORMATION:
; APPLICANT: MOORADIAN, DANIEL L.
; APPLICANT: FIELDS, GREGG B.
; TITLE OF INVENTION: METHOD FOR MODIFYING A SUBSTRATE SURFACE
; TITLE OF INVENTION: TO INCLUDE A BIOMOLECULE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
```


ADDRESSEE: MUEITING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
STREET: 119 NO. 5853/44th Fourth Street, Suite 203
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/699,965
FILING DATE: 20-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUEITING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00300101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-699-965-2

Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRAI 8

RESULT 5
US-08-435-149-6
Sequence 6, Application US/08435149
Patent No. 5866402
GENERAL INFORMATION:
APPLICANT: INNIS, MICHAEL A.
APPLICANT: ZAROR, ISABEL
APPLICANT: CREASEY, ABEL A.
TITLE OF INVENTION: CHIMERIC MCP AND DAP PROTEINS WITH CELL
TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
CITY: EMERYVILLE
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,149
FILING DATE: 05-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SAVERIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0989.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585

TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-435-149-6

Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRAI 8

RESULT 6
US-09-025-706-10
Sequence 10, Application US/09025706
Patent No. 5958874
GENERAL INFORMATION:
APPLICANT: Clark, Richard A
APPLICANT: Greiling, Doris
APPLICANT: Gallit, James
TITLE OF INVENTION: RECOMBINANT FIBRONECTIN-BASED
TITLE OF INVENTION: EXTRACELLULAR MATRIX FOR WOUND HEALING
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jackle Fleischmann & Mugel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,706
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87653.97R263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-025-706-10

Query Match 72.1%; Score 31; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QPPRAAI 7
Db 2 QPPRAI 8

RESULT 7

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US-08-394-748A-13
; Sequence 13, Application US/08394748A
; Patent No. 6013628
; GENERAL INFORMATION:
; APPLICANT: Skubitz, Amy P.N.
; APPLICANT: Furght Leo T.
; APPLICANT: Balles, Mark
; APPLICANT: Gregerson, Dale S.
; APPLICANT: Agarwal, Anita
; APPLICANT: Wright, Martha M.
; APPLICANT: Murali, Shobana
; TITLE OF INVENTION: Method for Treating Conditions of the Eye
; TITLE OF INVENTION: Using Polypeptides
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 6013628west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,748A
; FILING DATE: 27-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/203,458
; FILING DATE: 28-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 600.307US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; STRAIN: FN-C/H-V
US-08-394-748A-13

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

RESULT 8
US-08-916-913A-3
; Sequence 3, Application US/08916913A
; Patent No. 6121027
; GENERAL INFORMATION:
; APPLICANT: Clapper, David L.
; APPLICANT: Swanson, Melvin J.
; APPLICANT: Hu, Sheau-Ping
; APPLICANT: Amos, Richard A.
; APPLICANT: Everson, Terrence P.
; TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOIETIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Fredrikson & Byron, P.A.
; STREET: 900 Second Avenue South
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-3397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows-97
; SOFTWARE: ASCII files
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,913A
; FILING DATE: 15 August 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6121027e
; FILING DATE: No. 6121027e
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Philip M.
; REGISTRATION NUMBER: 31,162
; REFERENCE/DOCKET NUMBER: 9896.116.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 347-7088
; TELEFAX: (612) 347-7077
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-916-913A-3

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

RESULT 9
US-09-025-622-10
; Sequence 10, Application US/09025622
; Patent No. 6194378
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A.
; APPLICANT: Greiling, Doris
; TITLE OF INVENTION: FIBRONECTIN PEPTIDES-BASED EXTRACELLULAR
; TITLE OF INVENTION: MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaackle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,622
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bramer, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97E270
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-025-622-10

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

RESULT 10
US-08-847-065-11
; Sequence 11, Application US/08847065
; Patent No. 6245335
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; APPLICANT: Rosenow, Carsten I.
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Witzemann, Theresa M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; TITLE OF INVENTION: ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,065
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-158 ..
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-847-065-11

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

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Db 2 QPPRAAI 8

RESULT 11
US-08-960-054A-6
; Sequence 6, Application US/08960054A
; Patent No. 6261537
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/08/960,054A
; CURRENT FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-08-960-054A-6

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

RESULT 12
US-08-958-993A-6
; Sequence 6, Application US/08958993A
; Patent No. 6264917
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/993
; CURRENT APPLICATION NUMBER: US/08/958,993A
; CURRENT FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-08-958-993A-6

Query Match 72.1%; Score 31; DB 3; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
Db 2 QPPRAAI 8

RESULT 13
US-08-959-206A-2
; Sequence 2, Application US/08959206A
; Patent No. 6331289
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS

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; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/08/959,206A
; CURRENT FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fibronectin
; OTHER INFORMATION: peptide
US-08-959-206A-2

Query Match 72.1%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
DB 2 QPPRARI 8

RESULT 14
US-09-101-751A-58
; Sequence 58, Application US/09101751A
; Patent No. 6465253
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS
; FILE REFERENCE: 85710
; CURRENT APPLICATION NUMBER: US/09/101,751A
; CURRENT FILING DATE: 1999-01-23
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..{}
; OTHER INFORMATION: Description of Unknown Organism: Artificial
; OTHER INFORMATION: Sequence
US-09-101-751A-58

Query Match 72.1%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
DB 2 QPPRARI 8

RESULT 15
US-09-591-564-3
; Sequence 3, Application US/09591564
; Patent No. 6514734
; GENERAL INFORMATION:
; APPLICANT: Clapper, David L.
```

```
; Swanson, Melvin J.
; Hu, Sheau-Ping
; Amos, Richard A.
; Everson, Terrence P.
; TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH BIOLOGICALLY
; ACTIVE MOIETIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fredrikson & Byron, P.A.
; STREET: 900 Second Avenue South
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-3397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows-97
; SOFTWARE: ASCII files
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/591,564
; FILING DATE: 09-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/916,913
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Philip M.
; REGISTRATION NUMBER: 31,162
; REFERENCE/DOCKET NUMBER: 9896.116.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 347-7088
; TELEFAX: (612) 347-7077
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-591-564-3

Query Match 72.1%; Score 31; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPPRAAI 7
DB 2 QPPRARI 8

Search completed: July 28, 2004, 07:55:51
Job time : 18 secs
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